

In the Specification:

On page 46, please replace the paragraph beginning on line 24 with the following paragraph:

2. Two nucleic acid fragments are "homologous" if they are capable of hybridizing to one another under hybridization conditions described in Maniatis *et al.*, *op. cit.*, pp. 320-323. However, using the following wash conditions: 2 x SCGSSC, 0.1% SDS, room temperature twice, 30 minutes each; then 2 x SCGSSC, 0.1% SDS, 50° C once, 30 minutes; then 2 x SCGSSC, room temperature twice, 10 minutes each, homologous sequences can be identified that contain at most about 25-30% basepair mismatches. More preferably, homologous nucleic acid strands contain 15-25% basepair mismatches, even more preferably 5-15% basepair mismatches. These degrees of homology can be selected by using more stringent wash conditions for identification of clones from gene libraries (or other sources of genetic material), as is well known in the art.